

The Contribution of the International Rice Genebank (IRG) to Varietal Improvement and Farm Productivity in Eastern India

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Why we need the IRG

Rice is the most important cereal crop and the staple food of more than half the world's population with Asia representing the largest producing and consuming region. During the Green Revolution in the 1960s, high-yielding rice varieties were introduced in response to the specter of famine as population densities rose and productivity stagnated. This remarkably successful event had the unintended consequence that farmers rapidly replaced many traditional varieties and wild species with new varieties, leading to a loss in crop diversity. Genetic variation from traditional varieties and related wild species is needed in crop improvement to cope with the many biotic and abiotic stresses that challenge rice production—and is especially valuable with climate change.

HIGHLIGHTS

- One in five of the improved varieties cultivated on 95% of rice area in Eastern India (10.8 million hectares during the 2015 wet season) had at least one parent supplied directly by the IRG.
- According to Mendelian principles, almost half (45%) of the genetic composition of these improved rice varieties is derived from IRG accessions
- The average Coefficient of Parentage (COP) among the 10 most widely grown improved rice varieties is 9.7%, implying a high latent diversity conferred by genealogy
- A 10% increase in the definite genetic contribution of the IRG is associated with a 27% increase in rice yields

Over the past decades, the rice genetic resources maintained by the International Rice Genebank (IRG) have been used effectively to increase the productivity of the crop particularly among smallholder farm families in lower income countries. Rice genetic improvement using IRG accessions was

accomplished through IRR's breeding program which produces improved cultivars both in the form of "varieties" that are ready for use as parent material in national plant-breeding programs. The economic value of rice breeding has been demonstrated continuously over the past half-century. However,

BOX 1 The International Rice Genebank

The International Rice Research Institute (IRRI) initiated the collection of rice genetic resources in 1962 to protect against the loss of rice diversity. That effort eventually led to the establishment of the International Rice Genebank (IRG) in 1971. The IRG is located in the headquarters of IRRI in Los Baños, Laguna, Philippines. As of June 2018, the collection includes 130,139 accessions, comprising accessions of 123,837 *Oryza sativa*, 1,655 of *O. glaberrima*, and 4,647 wild relatives and interspecific hybrids. IRG has the largest and most diverse collection of rice genetic resources in the world and continues to grow as countries send seeds for conservation and sharing for common public good. It ensures that best practices are used to conserve this vital genetic resource, following the guidelines set by the Food and Agriculture Organization (FAO). It also carries out research to further reduce the risk of losing any of the genetic diversity. The IRG collection has duplicates as back-up in Fort Collins, Colorado, USA, and at the Svalbard Global Seed Vault in Norway.

The IRG shares seeds of small quantities free of charge on demand to any individual or organization anywhere in the world for the purposes



of research, breeding, or training for food and agriculture, using guidelines set by International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), under an agreement signed in October 2006. Over the past decades, the rice genetic resources maintained by the IRG have been used effectively to increase the productivity of the rice crop particularly among smallholder farm families in lower income countries.

other than the landmark studies by Gollin and Evenson, we are not aware of analyses that have explicitly related productivity changes on farm to genbank accessions through varietal improvement.

Our analysis provides renewed, evidence-based documentation of the value of the contribution of the IRG to rice productivity on farms in Eastern India. India is the world's second largest producer of rice. More than half of the population depends on rice as their staple food. Since 1976, IRG has been active in seed distribution in India. In fact, India ranks first among the top recipients of germplasm from IRG.

To test the effect of IRG ancestry, we propose an approach for attributing ancestry and estimate a yield response function with an econometric model. Next, we examine the country of origin of all IRG ancestors in the genealogies of improved rice varieties grown by the over 8000 farmers surveyed in 2016. We develop "profiles" of the three most popular progenitors. Lastly, we evaluate the genealogical (latent) diversity of the 10 most extensively grown, improved rice varieties using Coefficients of Parentage (COP).

Synopsis of methods

We use data collected in 2016 by IRRI from 8,640 rice farmers in 720 villages and four states of Eastern India (Eastern Uttar Pradesh, Bihar, Orissa and West Bengal) through a project called Rice Monitoring Survey (RMS), by Bill and Melinda Gates Foundation (BMGF).

The survey gathered information on the rice varieties cultivated by the farmers during the wet season (*kharif*) of 2015 and examined diffusion of submergence as well as drought tolerant rice varieties. Figure 1 shows the geographical location of the villages included in the survey.

To estimate the genetic contribution of the IRG, we began by identifying the most popular improved rice varieties. These covered 95% of the total area planted with improved rice varieties in Eastern India. We conducted a pedigree analysis using Mendelgram to quantify the progenitor contribution of IRG accessions to each improved rice variety. Mendelgram assumes that each parent contributed an equal amount to their progeny. We defined possible

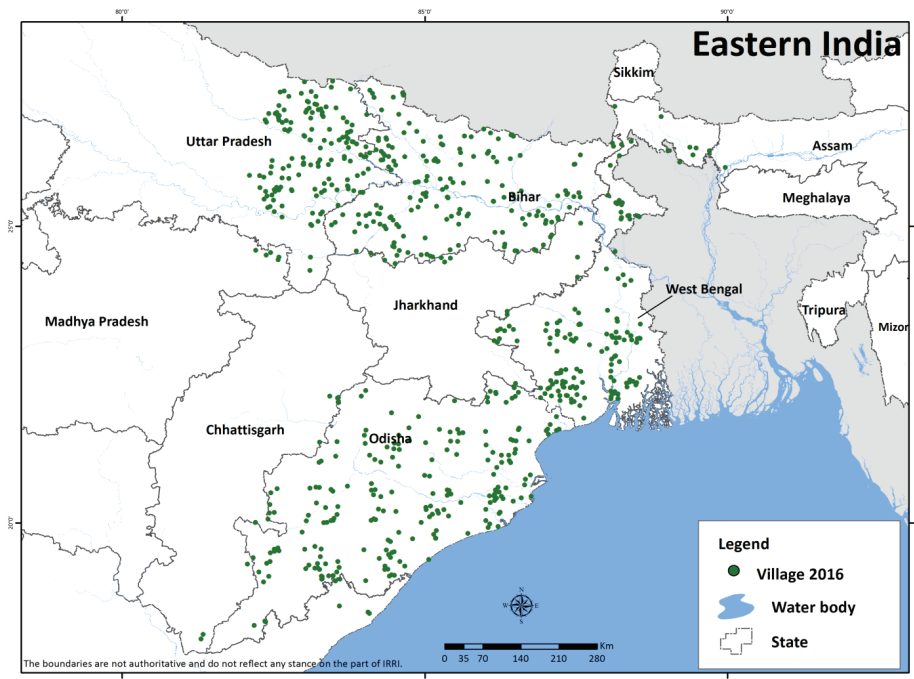


Figure 1. Geographical location of the sample villages of the Rice Monitoring Survey in 2016. Source: Rice Monitoring Survey (RMS) 2016 in India

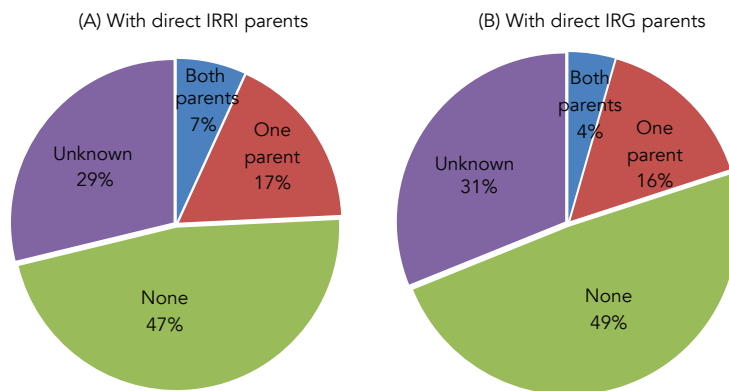


Figure 2. Distribution of most adopted rice varieties with direct IRRI and IRG parentages in Eastern India, 2015 wet season. Sources: Rice Monitoring Survey (RMS) 2016 in India and International Rice Information System (IRIS)

contribution as a progenitor that does not have an IRG collection number but has a match by name somewhere in the IRG collection. A definite contribution is a progenitor with an IRGC number.

The econometric model was a plot-level yield response function that controls for the influence of conventional inputs (fertilizer, labor, machinery, plant protection, irrigation), management (age, education, access to inputs, credit and extension advice), and environmental factors (submergence, salinity, drought). We estimated and compared the statistical fit of several functional forms.

The country of origin of the IRG accessions found in the ancestry of each variety was identified. Three of the most frequently used progenitors were "profiled" using detailed secondary

information. The COPs were computed for all pairwise combinations among the 10 most widely grown, improved rice varieties in order to evaluate the genealogical diversity present in farmers' fields. The genetic diversity conferred through genealogy is sometimes termed "latent" because it is not measured directly with molecular data.

Key findings

Nearly a quarter (24%) of the 132 improved rice varieties cultivated by farmers in Eastern India during the 2015 wet season had at least one IRRI parent (7% have both direct IRRI parents and 17% have only one direct IRRI parent, Figure 2A). Among these, 45 varieties were cultivated on about 10.78 million hectares which covered 95% of the total cultivated area of improved rice varieties. One out of five (20%) of these popular varieties have at least one

BOX 2 The Genebank Impacts Fellowship

The 2018 Genebank Impacts Fellowship Program aimed to provide evidence base for continued support to genebanks to ensure the availability of options for future plant breeders, scientists, and farmers, in view of increasing food demand from a growing world population in a changing climate. As one of the seven fellows, I was assigned to systematically evaluate the contribution of the International Rice Genebank (IRG) on improved rice varieties and farm productivity in Eastern India.

The “bootcamp” workshop organized by Crop Trust and the Genebank Platform as part of the fellowship program enhanced my knowledge on genebank operations and crop diversity conservation through the valuable information shared by impact assessment specialists and conservation scientists in the global CGIAR community.

The mentorship program of the fellowship intensified my capacity in shaping my research topic and work plans. Grace Capilit, database manager of IRG, provided me the pedigree data and helped me in computing the progenitor contribution of IRG in the identified rice varieties. The expertise of Melinda Smale and Nelissa Jamora contributed valuable inputs in the methodology, data analysis, and report writing.

My research under this fellowship is the first cross-cutting research between the Agri-food Policy Platform (APP) and IRG. My



Donald worked closely with the IRG manager Flora de Guzman.

collaboration with IRG creates possibilities of doing more research on impact assessment and policy on genetic resources in the future.

In addition, this fellowship became a great venue of gaining new friends with other fellows. We created a community of practice where we can share our experiences in doing our own research as well as significant moments of our personal lives.

direct parent from the IRG, cultivated on 43% of the total area (Figure 2B).

On average, based on Mendelian principles, 45% of the genetic composition of an improved rice variety cultivated by farmers during the 2015 wet season came from IRG accessions. The progenitor contribution increases to 77% if the possible contribution is added. These results serve as evidence of the significant contribution of IRG to the development of improved rice varieties in Eastern India.

The preferred, translog model shown in Table 1 indicates that the coefficient of the definite IRG contribution is positive and significant. Larger genetic contributions from IRG are significantly associated with higher on-farm yields of improved rice varieties. The size of the estimated coefficient suggests that on average, and controlling for other factors, a 10% increase in the definite IRG contribution is associated with a 27% yield increase. Our findings imply that the germplasm acquired from IRG contributed to the yield improvement of rice varieties grown by farmers in Eastern India during the 2015 wet season.

We identified 122 unique progenitors with definite and possible contribution

of IRG from 18 countries of origin. Philippines has the highest (35), followed by India (30). Peta, Dee Geo Woo Gen (DGWG), and Fortuna were the three most frequently used progenitors with definite IRG contribution.

We found an average COP of 0.0973—meaning that any pair of top 10 varieties grown by farmers has only 9.73% identical progenitors in their pedigrees. High genealogical (latent) diversity

among these varieties is likely the result of crossing germplasm from different countries of origin. Our evidence shows that IRG’s contribution is associated with both higher yields and higher genealogical diversity on farms in Eastern India. This is a “win-win” finding since often, higher yields across a farming landscape are postulated to be associated with lower diversity among varieties grown by farmers.

Table 1. Estimation results of the final yield response function, 2015 wet season, Eastern India.

Independent variables	Coef.	Independent variables	Coef.
Fertilizer (lnFer)	α_1 0.869**	Crop_establishment	0.315**
Labor (lnLab)	α_2 -0.673*	Submergence	-2.469**
Power_cost (lnPow)	α_3 0.139	Salinity	-1.279*
Other_inputs (lnOth)	α_4 0.206**	Drought	-1.247**
lnFer x lnFer	α_{11} -0.034*	Age	-0.013
lnLab x lnLab	α_{22} 0.236**	Age x Age	0.000
lnPow x lnPow	α_{33} -0.002	Education	-0.017
lnOth x lnOth	α_{44} 0.015**	Education x Education	0.002
lnFer x lnLab	α_{12} -0.088*	Access_input	-0.244*
lnFer x lnPow	α_{13} 0.027**	Access_credit	0.305*
lnFer x lnOth	α_{14} -0.040**	Access_extworker	-0.128
lnLab x lnPow	α_{23} -0.055**	IRG_contribution	0.027**
lnLab x lnOth	α_{24} -0.034**	i.State	included
lnPow x lnOth	α_{34} 0.013**	Constant	4.764**
Irrigation_percent	0.127**		

No. of observations = 8,967 | Dependent variable = yield (kg/ha)
** significant at 1%, *significant at 5%



Conclusion and future considerations

Our analysis adds new evidence to research conducted several decades ago concerning the value of the IRG. We have demonstrated the genetic contribution of the IRG to the development of improved rice varieties and rice productivity on farms in Eastern India. This was achieved while also contributing to high genealogical diversity among cultivated varieties. Findings illustrate the benefits of conserving, maintaining and distributing rice genetic resources by the IRG.

For future research, the total monetary contribution of IRG can be estimated for the whole Eastern India, considering the estimated yield gain attributable to the progenitor IRG contribution in an

improved rice variety. Due to the availability of similar data in Bangladesh, a similar case study will also be conducted in this country to assess the farm-level impact of IRG. Another country study will add a different perspective and may reveal new insights concerning the impact of IRG.

Further reading

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Additional details can be found in the paper on which this brief is based: Villanueva, Donald, Grace Lee Capilit, Melinda Smale, Nelissa Jamora and Ruairadh Sackville Hamilton. 2019. The contribution of the International Rice Genebank (IRG) to varietal improvement and farm productivity in Eastern India. Genebank Impacts Working paper No. 3. CGIAR Genebank Platform, IRRI, and the Crop Trust.

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